

10/030549

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SEQUENCE LISTING

<110> SOLVAY PHARMACEUTICALS B.V.

5 <120> Novel human G-protein coupled receptor

<130> SPW99.04

<140>

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<160> 18

15 <170> PatentIn Ver. 2.1

<210> 1

<211> 1659

<212> DNA

<213> Homo sapiens

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<220>

<221> CDS

<222> (36)...(1559)

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				1				5		

aac	agc	acg	cgc	gag	agt	aac	agc	acg	cac	acg	tgc	atg	ccc	ctc	tcc	101
Asn	Ser	Thr	Arg	Glu	Ser	Asn	Ser	Ser	His	Thr	Cys	Met	Pro	Leu	Ser	
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aaa	atg	ccc	atc	agc	ctg	gcc	cac	ggc	atc	atc	cgc	tca	acc	gtg	ctg	149
Lys	Met	Pro	Ile	Ser	Leu	Ala	His	Gly	Ile	Ile	Arg	Ser	Thr	Val	Leu	
25						30						35				

gtt	atc	ttc	ctc	gcc	gcc	tct	ttc	gtc	ggc	aac	ata	gtg	ctg	gcg	cta	197
Val	Ile	Phe	Leu	Ala	Ala	Ser	Phe	Val	Gly	Asn	Ile	Val	Leu	'Ala	Leu	
40						45				50						

gtg	ttg	cag	cgc	aag	ccg	cag	ctg	ctg	cag	gtg	acc	aac	cgt	ttt	atc	245
Val	Leu	Gln	Arg	Lys	Pro	Gln	Leu	Leu	Gln	Val	Thr	Asn	Arg	Phe	Ile	
55					60				65		70					

ttt	aac	ctc	ctc	gtc	acc	gac	ctg	ctg	cag	att	tcg	ctc	gtg	gcc	ccc	293
Phe	Asn	Leu	Leu	Val	Thr	Asp	Leu	Leu	Gln	Ile	Ser	Leu	Val	'Ala	Pro	
75					80				85							

50	tgg	gtg	gtg	gcc	acc	tct	gtg	cct	ctc	ttc	tgg	ccc	ctc	aac	agc	cac	341
Trp	Val	Val	Ala	Thr	Ser	Val	Pro	Leu	Phe	Trp	Pro	Leu	Asn	Ser	His		
90					95					100							

55

	ttc tgc acg gcc ctg gtt agc ctc acc cac ctg ttc gcc ttc gcc agc Phe Cys Thr Ala Leu Val Ser Leu Thr His Leu Phe Ala Phe Ala Ser 105 110 115	389
5	gtc aac acc att gtc ttg gtg tca gtg gat cgc tac ttg tcc atc atc Val Asn Thr Ile Val Leu Val Ser Val Asp Arg Tyr Leu Ser Ile Ile 120 125 130	437
10	cac cct ctc tcc tac ccg tcc aag atg acc cag cgc cgc ggt tac ctg His Pro Leu Ser Tyr Pro Ser Lys Met Thr Gln Arg Arg Gly Tyr Leu 135 140 145 150	485
15	ctc ctc tat ggc acc tgg att gtg gcc atc ctg cag agc act cct cca Leu Leu Tyr Gly Thr Trp Ile Val Ala Ile Leu Gln Ser Thr Pro Pro 155 160 165	533
20	ctc tac ggc tgg ggc cag gct gcc ttt gat gag cgc aat gct ctc tgc Leu Tyr Gly Trp Gly Gln Ala Ala Phe Asp Glu Arg Asn Ala Leu Cys 170 175 180	581
	tcc atg atc tgg ggg gcc agc ccc agc tac act att ctc agc gtc gtc Ser Met Ile Trp Gly Ala Ser Pro Ser Tyr Thr Ile Leu Ser Val Val 185 190 195	629
25	tcc ttc atc gtc att cca ctg att gtc atg att gcc tgc tac tcc gtc Ser Phe Ile Val Ile Pro Leu Ile Val Met Ile Ala Cys Tyr Ser Val 200 205 210	677
30	gtg ttc tgt gca gcc cgg agg cag cat gct ctg ctg tac aat gtc aag Val Phe Cys Ala Ala Arg Arg Gln His Ala Leu Leu Tyr Asn Val Lys 215 220 225 230	725
35	aga cac agc ttg gaa gtc cga aag gac tgt gtc gag aat gag gat Arg His Ser Leu Glu Val Arg Val Lys Asp Cys Val Glu Asn Glu Asp 235 240 245	773
40	gaa gag gga gca gag aag gag gag ttc cag gat gag agt gag ttt Glu Glu Gly Ala Glu Lys Lys Glu Glu Phe Gln Asp Glu Ser Glu Phe 250 255 260	821
	cgc cgc cag cat gaa ggt gtc aag gcc aag gag ggc aga atg gaa Arg Arg Gln His Glu Gly Glu Val Lys Ala Lys Glu Gly Arg Met Glu 265 270 275	869
45	gcc aag gac ggc agc ctg aag gcc aag gaa gga agc acg ggg acc agt Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu Gly Ser Thr Gly Thr Ser 280 285 290	917
50	gag agt agt gta gag gcc agg ggc agc gag gag gtc aga gag agc agc Glu Ser Ser Val Glu Ala Arg Gly Ser Glu Glu Val Arg Glu Ser Ser 295 300 305 310	965
55	acg gtg gcc agc gac ggc agc atg gag ggt aag gaa ggc agc acc aaa Thr Val Ala Ser Asp Gly Ser Met Glu Gly Lys Glu Gly Ser Thr Lys 315 320 325	1013

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	gtt gag gag aac agc atg aag gca gac aag ggt cgc aca gag gtc aac	1061		
	Val Glu Glu Asn Ser Met Lys Ala Asp Lys Gly Arg Thr Glu Val Asn			
5	330	335	340	
	cag tgc agc att gac ttg ggt gaa gat ggc atg gag ttt ggt gaa gac	1109		
	Gln Cys Ser Ile Asp Leu Gly Glu Asp Gly Met Glu Phe Gly Glu Asp			
	345	350	355	
10	gac atc aat ttc agt gag gat gac gtc gag gca gtg aac atc ccg gag	1157		
	Asp Ile Asn Phe Ser Glu Asp Asp Val Glu Ala Val Asn Ile Pro Glu			
	360	365	370	
15	agc ctc cca ccc agt cgt cgt aac aac agc aac cct cct ctg ccc	1205		
	Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn Ser Asn Pro Pro Leu Pro			
	375	380	385	390
20	agg tgc tac cag tgc aaa gct gct aaa gtg atc ttc atc atc att ttc	1253		
	Arg Cys Tyr Gln Cys Lys Ala Ala Lys Val Ile Phe Ile Ile Ile Phe			
	395	400	405	
25	tcc tat gtg cta tcc ctg ggg ccc tac tgc ttt tta gca gtc ctg gcc	1301		
	Ser Tyr Val Leu Ser Leu Gly Pro Tyr Cys Phe Leu Ala Val Leu Ala			
	410	415	420	
30	gtg tgg gtg gat gtc gaa acc cag gta ccc cag tgg gtg atc acc ata	1349		
	Val Trp Val Asp Val Glu Thr Gln Val Pro Gln Trp Val Ile Thr Ile			
	425	430	435	
35	atc atc tgg ctt ttc ttc ctg cag tgc tgc atc cac ccc tat gtc tat	1397		
	Ile Ile Trp Leu Phe Leu Gln Cys Cys Ile His Pro Tyr Val Tyr			
	440	445	450	
40	ggc tac atg cac aag acc att aag aag gaa atc cag gac atg ctg aag	1445		
	Gly Tyr Met His Lys Thr Ile Lys Lys Glu Ile Gln Asp Met Leu Lys			
	455	460	465	470
45	aag ttc ttc tgc aag gaa aag ccc ccg aaa gaa gat agc cac cca gac	1493		
	Lys Phe Phe Cys Lys Glu Lys Pro Pro Lys Glu Asp Ser His Pro Asp			
	475	480	485	
50	ctg ccc gga aca gag ggt ggg act gaa ggc aag att gtc cct tcc tac	1541		
	Leu Pro Gly Thr Glu Gly Gly Thr Glu Gly Lys Ile Val Pro Ser Tyr			
	490	495	500	
	gat tct gct act ttt cct tgaagtttagt tctaaggcaa accttgaaaa	1589		
	Asp Ser Ala Thr Phe Pro			
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55	tcagtcccttc agccacagct attttagagct ttaaaaactac caggttcaat cactggttat	1649		
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20 25 30
Ile Arg Ser Thr Val Leu Val Ile Phe Leu Ala Ala Ser Phe Val Gly
35 40 45
15 Asn Ile Val Leu Ala Leu Val Leu Gln Arg Lys Pro Gln Leu Leu Gln
50 55 60
20 Val Thr Asn Arg Phe Ile Phe Asn Leu Leu Val Thr Asp Leu Leu Gln
65 70 75 80
Ile Ser Leu Val Ala Pro Trp Val Val Ala Thr Ser Val Pro Leu Phe
85 90 95
25 Trp Pro Leu Asn Ser His Phe Cys Thr Ala Leu Val Ser Leu Thr His
100 105 110
Leu Phe Ala Phe Ala Ser Val Asn Thr Ile Val Leu Val Ser Val Asp
115 120 125
30 Arg Tyr Leu Ser Ile Ile His Pro Leu Ser Tyr Pro Ser Lys Met Thr
130 135 140
35 Gln Arg Arg Gly Tyr Leu Leu Leu Tyr Gly Thr Trp Ile Val Ala Ile
145 150 155 160
Leu Gln Ser Thr Pro Pro Leu Tyr Gly Trp Gly Gln Ala Ala Phe Asp
165 170 175
40 Glu Arg Asn Ala Leu Cys Ser Met Ile Trp Gly Ala Ser Pro Ser Tyr
180 185 190
Thr Ile Leu Ser Val Val Ser Phe Ile Val Ile Pro Leu Ile Val Met
195 200 205
45 Ile Ala Cys Tyr Ser Val Val Phe Cys Ala Ala Arg Arg Gln His Ala
210 215 220
50 Leu Leu Tyr Asn Val Lys Arg His Ser Leu Glu Val Arg Val Lys Asp
225 230 235 240
Cys Val Glu Asn Glu Asp Glu Glu Gly Ala Glu Lys Lys Glu Glu Phe
245 250 255
55

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Gln Asp Glu Ser Glu Phe Arg Arg Gln His Glu Gly Glu Val Lys Ala
260 265 270

5 Lys Glu Gly Arg Met Glu Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu
275 280 285

Gly Ser Thr Gly Thr Ser Glu Ser Ser Val Glu Ala Arg Gly Ser Glu
290 295 300

10 Glu Val Arg Glu Ser Ser Thr Val Ala Ser Asp Gly Ser Met Glu Gly
305 310 315 320

Lys Glu Gly Ser Thr Lys Val Glu Asn Ser Met Lys Ala Asp Lys
15 325 330 335

Gly Arg Thr Glu Val Asn Gln Cys Ser Ile Asp Leu Gly Glu Asp Gly
340 345 350

20 Met Glu Phe Gly Glu Asp Asp Ile Asn Phe Ser Glu Asp Asp Val Glu
355 360 365

Ala Val Asn Ile Pro Glu Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn
25 370 375 380

Ser Asn Pro Pro Leu Pro Arg Cys Tyr Gln Cys Lys Ala Ala Lys Val
385 390 395 400

Ile Phe Ile Ile Ile Phe Ser Tyr Val Leu Ser Leu Gly Pro Tyr Cys
30 405 410 415

Phe Leu Ala Val Leu Ala Val Trp Val Asp Val Glu Thr Gln Val Pro
420 425 430

35 Gln Trp Val Ile Thr Ile Ile Trp Leu Phe Phe Leu Gln Cys Cys
435 440 445

Ile His Pro Tyr Val Tyr Gly Tyr Met His Lys Thr Ile Lys Lys Glu
40 450 455 460

Ile Gln Asp Met Leu Lys Lys Phe Phe Cys Lys Glu Lys Pro Pro Lys
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<212> DNA

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50 <210> 10
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45 <220>
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